AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

LISTING OF CLAIMS:

Claim 1 (Original): A chimeric gene comprising the following operably linked DNA:

(a) a plant-expressible promoter;

(b) a DNA region which when transcribed yields a double-stranded RNA molecule capable of reducing the expression of an essential gene of a plant sap-sucking insect, said RNA molecule comprising a first and second RNA region wherein:

(i) said first RNA region comprises a nucleotide sequence of at least 19 consecutive nucleotides having at least about 94% sequence identity to the nucleotide sequence of said endogenous gene ;

(ii) said second RNA region comprises a nucleotide sequence complementary to said at least 19 consecutive nucleotides of said first RNA region;

(iii) said first and second RNA region are capable of base-pairing to form a double stranded RNA molecule between at least said 19 consecutive nucleotides of said first and second region;

(c) optionally, a 3' end region comprising transcription termination and polyadenylation signals functioning in cells of said plant.

Claim 2 (Currently Amended): The chimeric gene of claim 1, wherein said essential of said plant sap-sucking insect is selected from the group consisting of ~~the~~ genes encoding the following: a gut cell protein, a membrane protein, an ecdyson receptor, a γATPase, an

amino acid transporter, a transcription factor, a peptidylglycine alpha-amidating monooxygenase; a cystein protease, an aminopeptidase, a dipeptidase, a sucrase/ transglucosidase, a translation elongation factor, ~~the~~ an eucaryotic translation initiation factor 1A, a splicing factor, an apoptosis inhibitor; a tubulin protein, an actin protein, an alpha-actinin protein, a histone, a histone deacetylase, a cell cycle regulatory protein, a cellular respiratory protein; a receptor for an insect-specific hormonal signal, a juvenile hormone receptor, an insect peptidic hormone receptor; a protein regulating ion balance in ~~the~~ a cell, a proton-pump, a Na/K pump, an intestinal protease; an enzyme involved in sucrose metabolism, a digestive enzyme, a trypsin-like protease and a cathepsin B-like protease.

Claim 3 (Currently Amended): The chimeric gene of ~~claims 1 or 2~~ claim 1, wherein said double-stranded RNA silences the gene corresponding to the DNA sequence of any one of SEQ ID NO: 5 to 8, SEQ ID NO: 11 or SEQ ID NO: 12.

Claim 4 (Currently Amended): The chimeric gene of ~~any one of claims 1 to 3~~ claim 1, wherein between said first and second RNA region, a spacer region containing a plant intron is present.

Claim 5 (Currently Amended): The chimeric gene of ~~any one of claim 1 to 4~~ claim 1, wherein said essential gene has a portion which occurs with the same sequence or with at least 94 % sequence identity in homologous genes of several plant sap-sucking insects.

Claim 6 (Currently Amended): The chimeric gene of ~~any one of claim 1 to 5~~ claim 1, wherein said promoter is a constitutive promoter.

Claim 7 (Currently Amended): The chimeric gene of ~~any one of claim 1 to 6~~ claim 1, wherein said promoter is a vascular-specific or a phloem-specific promoter.

Claim 8 (Currently Amended): The chimeric gene of claim 7, wherein vascular- or phloem-specific promoter is selected from the group consisting of: ~~the~~ a rolC or rolA promoter of Agrobacterium rhizogenes, ~~the~~ a promoter of ~~the~~ a Agrobacterium tumefaciens T-DNA gene 5, the rice sucrose synthase RSs1 gene promoter, ~~the~~ a *Commelina* yellow mottle badnavirus promoter, ~~the~~ a coconut foliar decay virus promoter, ~~the~~ a rice tungro bacilliform virus promoter, the promoter of ~~the~~ a pea glutamine synthase GS3A gene, ~~the~~ a *invCD111* and *invCD141* promoters of ~~the~~ a potato invertase genes, ~~the~~ a promoter isolated from Arabidopsis shown to have phloem-specific expression in tobacco ~~by Kertbundit et al (1991)~~, ~~the~~ a VAHOX1 promoter region, ~~the~~ a pea cell wall invertase gene promoter, an acid invertase gene promoter from carrot, ~~the~~ a promoter of ~~the~~ a sulfate transporter gene *Sultr1;3*, ~~the~~ a promoter of a plant sucrose synthase gene, ~~the~~ a promoter of a plant sucrose transporter gene.

Claim 9 (Currently Amended): A plant cell, tissue, or a plant or a plant seed comprising the chimeric gene ~~of any one of claims 1 to 8~~ or the double-stranded RNA molecule described in ~~any one of claims 1 to 8~~ claim 1.

Claim 10 (Original): A method to silence a gene of a plant sap-sucking insect, comprising applying to the feed of said plant sap-sucking insect unpackaged, naked dsRNA or siRNA which is targeted to an essential plant sap-sucking gene.

Claim 11 (Original): The method of claim 10, wherein said essential gene is any of the genes listed in claim 2 above.

Claim 12 (Original): The method of claim 10, wherein said application is by expression of a dsRNA chimeric gene in phloem cells of a plant.

Claim 13 (Original): A method to silence a gene in an plant sap-sucking insect, comprising: adding naked, unpackaged dsRNA or siRNA to the diet or feed of said plant sap-sucking insect, wherein said dsRNA or siRNA targets said gene.

Claim 14 (Original): A method of controlling plant sap-sucking insects, comprising expressing in the phloem of a plant dsRNA that targets an essential plant sap-sucking insect gene.

Claim 15 (Original): The method of claim 14 wherein said gene is a gene expressed at least in the intestine or in gut cells.

Claim 16 (Original): The method of claim 14 wherein said plant sap-sucking insect is an aphid or a whitefly.

Claim 17 (Original): A plant, comprising stably inserted in its genome, the chimeric gene of claim 1, so that said chimeric gene is expressed in the phloem or xylem of said plant.

Claim 18 (Original): A method of identifying gene function in a plant sap-sucking insect, comprising the step of applying naked, unpackaged dsRNA targeting a plant sap-sucking insect gene to the diet of said insect, and evaluating phenotypic or biochemical changes in said insect.

Claim 19 (Original): A method of identification of novel targets for insecticidal compounds, comprising the steps of: a) applying naked, unpackaged dsRNA or siRNA molecules to the feed or diet of a plant-sap sucking insect; b) analyzing which genes when silenced confer lethality to said insect, c) cloning and characterizing said genes thus analyzed; d) identifying compounds that disrupt or inactivate said gene or the RNA or protein encoded thereby; and e) contacting said compounds with said insect or feed or diet of said insect to confirm the pesticidal nature of said compound.

Claim 20 (Original): Phloem of a plant, comprising siRNA targeted to an aphid essential gene.

Claim 21 (Original): Phloem sap of a plant, comprising siRNA targeted to an aphid essential gene.

Claim 22 (Original): An aphid gene comprising the sequence of any one of SEQ ID NO:5 to 8, SEQ ID NO: 11 or SEQ ID NO:12.

Claim 23 (Currently Amended): The method of claim 18 ~~or 19~~, wherein a cationic oligopeptide is mixed in the diet together with the dsRNA.

Claim 24 (Original): The method of claim 23, wherein said oligopeptide is a 12 amino acids poly-Arginine peptide.

Claim 25 (Currently Amended): The plant cell, tissue, plant or plant seed of ~~claims 9 or 17~~claim 9, which also comprises a chimeric gene encoding a cationic oligopeptide.

Claim 26 (Original): The plant cell, tissue, plant or plant seed of claim 25, wherein said oligopeptide is a 12 amino acids poly-Arginine peptide.

Claim 27 (New): The method of claim 19, wherein a cationic oligopeptide is mixed in the diet together with the dsRNA.

Claim 28 (New): The plant cell, tissue, plant or plant seed of claim 17, which also comprises a chimeric gene encoding a cationic oligopeptide.